

Patent claims

1. Genetically modified plant cell, characterised in that it has an increased activity of at least one Class 3 branching enzyme in comparison with corresponding **wild** type plant cells that have not been genetically modified.
2. Genetically modified plant cell according to Claim 1, wherein the genetic modification consists in the introduction of at least one foreign nucleic acid molecule into the genome of the plant.
3. Genetically modified plant cell according to Claim 2, wherein the foreign nucleic acid molecule codes a Class 3 branching enzyme.
4. Genetically modified plant cell according to Claim 3, wherein the said foreign nucleic acid molecule is chosen from the group consisting of
 - a) Nucleic acid molecules, which code a protein with the amino acid sequence given under Seq ID NO 4;
 - b) Nucleic acid molecules, which code a protein, the amino acid sequence of which has an identity of at least 50% with the amino acid sequence given under SEQ ID NO: 4;
 - c) Nucleic acid molecules, which include the nucleotide sequence shown under Seq ID NO 3 or a complimentary sequence;
 - d) Nucleic acid molecules, the nucleic acid sequence of which has an identity of at least 50% with the nucleic acid sequences described under a) or c);
 - e) Nucleic acid molecules, which hybridise with at least one strand of the nucleic acid molecules described under a) or c) under stringent conditions;
 - f) Nucleic acid molecules, the nucleotide sequence of which deviates from the

sequence of the nucleic acid molecules identified under a), b), c), d), e) or f) due to the degeneration of the genetic code; and

g) Nucleic acid molecules, which represent fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).

5. Genetically modified plant cell according to one of Claims 2 to 4, wherein the said foreign nucleic acid molecule is chosen from the group consisting of

a) T-DNA molecules, which lead to an increase in the expression of a Class 3 branching enzyme gene due to integration in the vegetable genome (T-DNA activation tagging);

b) DNA molecules, which contain transposons, which lead to an increase in the expression of a Class 3 branching enzyme gene due to integration in the vegetable genome (transposon activation tagging);

c) DNA molecules, which code a Class 3 branching enzyme and which are linked with regulatory sequences, which guarantee transcription in vegetable cells and lead to an increase in Class 3 branching enzyme activity in the cell.

d) Nucleic acid molecules introduced by means of in vivo mutagenesis, which lead to a mutation or an insertion of a heterologous sequence in at least one endogenous gene coding a Class 3 branching enzyme, wherein the mutation or insertion effects an increase in the expression of a gene coding a Class 3 branching enzyme.

6. Plant cell according to one of Claims 1 to 5, which synthesises a modified starch in comparison with corresponding wild type plant cells that have not been genetically modified.

7. Plant containing plant cells according to one of Claims 1 to 6.

8. Plant according to Claim 7, which is a starch-storing plant.

9. Plant according to Claim 7, which is a maize, rice, wheat, rye, oat, barley, cassava,

potato, sago, mung bean, pea or sorghum plant.

10. Plant according to Claim 9, which is a potato plant.
11. Propagation material of plants according to one of Claims 7 to 10, containing plant cells according to one of Claims 1 to 6.
12. Harvestable plant parts of plants according to one of Claims 7 to 10, containing plant cells according to one of Claims 1 to 6.
13. Method for the manufacture of a genetically modified plant according to one of Claims 7 to 10, wherein
 - a) a plant cell is genetically modified, whereby the genetic modification leads to an increase in the activity of a Class 3 vegetable branching enzyme in comparison with corresponding wild type plant cells that have not been genetically modified;
 - b) a plant is regenerated from plant cells from Step a); and
 - c) if necessary, further plants are produced with the help of the plants according to Step b).
14. Method according to Claim 13, wherein the genetic modification consists in the introduction of a foreign nucleic acid molecule into the genome of the plant.
15. Method according to Claim 14, wherein the said foreign nucleic acid molecule is chosen from the group consisting of
 - a) Nucleic acid molecules, which code a protein with the amino acid sequence given under Seq ID NO 4;
 - b) Nucleic acid molecules, which code a protein, the amino acid sequence of which has an identity of at least 50% with the amino acid sequence given under SEQ ID NO: 4;
 - c) Nucleic acid molecules, which include the nucleotide sequence shown under Seq ID NO 3 or a complimentary sequence;

- d) Nucleic acid molecules, the nucleic acid sequence of which has an identity of at least 50% with the nucleic acid sequences described under a) or c);
- e) Nucleic acid molecules, which hybridise with at least one strand of the nucleic acid molecules described under a) or c) under stringent conditions;
- f) Nucleic acid molecules, the nucleotide sequence of which deviates from the sequence of the nucleic acid molecules identified under a), b), c), d), e) or f) due to the degeneration of the genetic code; and
- g) Nucleic acid molecules, which represent fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).

16. Method according to Claim 14, wherein the said foreign nucleic acid molecule is chosen from the group consisting of

- a) T-DNA molecules, which lead to an increase in the expression of a Class 3 branching enzyme gene due to integration in the vegetable genome (T-DNA activation tagging);
- b) DNA molecules, which contain transposons, which lead to an increase in the expression of a Class 3 branching enzyme gene due to integration in the vegetable genome (transposon activation tagging);
- c) DNA molecules, which code a Class 3 branching enzyme and which are linked with regulatory sequences, which guarantee transcription in vegetable cells and lead to an increase in Class 3 branching enzyme activity in the cell;
- d) Nucleic acid molecules introduced by means of in vivo mutagenesis, which lead to a mutation or an insertion of a heterologous sequence in at least one endogenous gene coding a Class 3 branching enzyme, wherein the mutation or insertion effects an increase in the expression of a gene coding a Class 3 branching enzyme.

17. Method according to one of Claims 13 to 16, wherein the genetically modified plant synthesises a modified starch in comparison with corresponding wild type plants that have not been genetically modified.

18. Modified starch obtainable from a genetically modified plant according to one of Claims 7 to 10, from propagation material according to Claim 11, or from harvestable plant parts according to Claim 12.
19. Method for the manufacture of a modified starch including the step of extracting the starch from a plant cell according to one of Claims 1 to 6.
20. Method for the manufacture of a modified starch including the step of extracting the starch from a plant according to one of Claims 7 to 10.
21. Method for the manufacture of a modified starch including the step of extracting the starch from harvestable plant parts according to Claim 12.
22. Method for the manufacture of a derived starch, wherein modified starch according to Claim 18 or obtainable by means of a method according to one of Claims 19, 20 or 21 is derived.
23. Use of genetically modified plants according to one of Claims 7 to 10 for the manufacture of a modified starch.
24. Modified starch obtainable by means of a method according to one of Claims 19, 20 or 21.
25. Derived starch obtainable by means of a method according to Claim 22.
26. Use of modified starch according to one of Claims 18 or 24 for the manufacture of derived starch.